

HYPERSENSITIVE RESPONSE: “A PLAYER IN PLANT DEFENSE”

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ABSTRACT

Plants have developed sophisticated mechanisms to protect themselves from various diseases. Besides preformed physical and chemical barrier that hinders infection, a wide range of defence responses are induced only after pathogen attack. These responses include translocation of Ca^{2+} and protons across the plasma membrane into the cytosol, hypersensitive response, protein phosphorylation/ dephosphorylation, activation of enzymes that generate ROS such as NADPH-oxidase and peroxidase, accumulation of NO and SA and expression of defense related genes. Hypersensitive response is one of the immediate defence mechanisms of plant against pathogen infection. It is a form of programmed cell death (PCD) that helps in restricting the pathogen growth. Present review includes the role of hypersensitive response in defense, molecular marker of hypersensitive response and the components of major signalling pathways that play an important role in defence. This review will give us an insight on hypersensitive response (HR) of plants with respect to the physiological, biochemical and molecular determinants in different plant species.

KEYWORDS: *Hypersensitive Response, Map Kinase, SAR, Plant Defence and HSR203J*

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INTRODUCTIONS

Plants are a source of food and shelter by a wide range of microorganisms including viruses, bacteria, nematodes and insects. Many of these microbes act as pathogens that impair plant growth and development. However, plants have developed diverse strategies to defend themselves. They respond to infection using two-branched innate immune system. The first branch uses trans-membrane pattern recognition receptors (PRR) that responds to slowly evolving microbial or pathogen-associated molecular pattern (PAMP) such as flagellin or chitin, a component of fungal cell walls (Jones and Dangl, 2006). During interaction with virulent parasites, PRRs confer weak immune responses that attenuates pathogen growth and contribute to basal defence. Reduced PAMP-mediated defence probably results from successful host defence suppression by pathogen effectors. The second branch acts largely through protein products encoded by most Resistance genes (*R* genes) (Jones and Dangl, 2006). Resistance (*R*) proteins represents mainly intracellular, immune receptor class having the capacity to directly or indirectly detect isolate-specific pathogen effectors, encoded by avirulence (*avr*) genes. Recognition requires the presence of matching *avr* and *R* genes in the two species and is thought to be mediated by ligand receptor binding (Glazebrook, 1999). Efforts have been made to elucidate plant-pathogen interaction leading to the identification and cloning of several *avr* and *R* genes (Keen and Staskawicz, 1998; Dangl, 1995). In conclusion, the multi-component response of plants to pathogens in host and non-host resistance appears to be activated by ligand receptor interactions, in which *avr* gene products and PAMPs serve as ligands for plasma membrane located or cytosolic receptors (Odjakova and Hadjiivanova, 2001).

Receptor mediated recognition initiates cellular and systemic signaling processes that activate

multicomponent defense responses at local and systemic levels resulting in rapid establishment of local resistance and delayed development of systemic acquired resistance (Scheel, 1998). The earliest reactions of plant cells include change in plasma membrane permeability leading to Ca^{2+} and proton influx and K^{+} and Cl^{-} efflux (Mc Dowell and Dangl, 2000). Ion fluxes subsequently induce production of reactive oxygen species (ROS), such as superoxide (O_2^{-}), hydrogen peroxide (H_2O_2) and hydroxyl free radical (OH^{\cdot}). Localized production of ROS and nitric oxide (NO) acts as second messenger for HR induction and defense gene expression (Piffanelli *et al.*, 1999). In systemic defense, signal is mediated by several molecules which function as messengers in plants, for example, salicylic acid (SA) and jasmonic acid (JA), or even volatiles such as NO and ethylene (ET) (Baker *et al.*, 1997). These messengers interact with specific binding proteins that are implicated in the transcriptional activation of pathogenesis related genes in response to pathogen aggression including hypersensitive response (Montesinos *et al.*, 2002).

This review aims to summarize some of the recent findings on hypersensitive response, the physiological, biochemical and molecular machineries of the HR. Role of elicitors, reactive oxygen species is also discussed. Present review also includes MAP kinase, a component of the signalling pathway. As HR is a form of programmed cell death (PCD) associated with plant response to pathogens, a description of main morphological and biochemical determinants of PCD is also discussed.

Hypersensitive Response (HR)

Among the vast array of defense strategies to combat the disease, the most efficient and immediate resistance reaction against pathogen attack is the hypersensitive response. HR is defined as “the rapid death of plant cells in association with restriction of pathogen growth” (Good man and Novacky, 1994). It is recognized by the presence of brown, dead cells at the site of infection. Klement (1971; 1986) defined three phases in the HR to plant pathogenic bacteria:

- **INDUCTION PHASE**, requiring the presence of living bacteria in the intercellular spaces. Avirulence (*avr*) genes are activated in bacteria and the *avr* gene products are delivered directly into the host cells by a special secretory mechanism.
- **LATENT PHASE**, during which living bacteria is no longer required. No macroscopic symptoms occur during this phase, but changes in the physiology of the plant cells can be detected. During this phase the irreversible membrane damage associated with the HR occurs.
- **PRESENTATION or COLLAPSE PHASE**, during which host cells in the inoculated region collapse and desiccate.

However, the duration of these three phases depends upon the host pathogen combination and the environmental conditions.

HR accompanies “incompatible interaction” and has been thought to play important role in disease resistance. Recent studies have shown that hypersensitive response is an active process and is a form of programmed cell death (Greenberg, 1997). The hypersensitive response occurs as a result of initial identification events between host and pathogen, which are mediated by the plant resistance (R) and microbial avirulence (*avr*) genes (Flor, 1971). In case of

biotrophs, HR mediated cell death alone is sufficient to restrict the pathogen infection. In an interaction with obligate biotrophic pathogens that form historical associations with host cells, plant cell death would deprive the pathogen of access to further nutrients. However, the role of HR is less clear in necrotrophs (**Hammond-Kosack and Jones, 1996**). The HR may cause pathogen arrest, but may also occur as a consequence of the activation of other defense response. Most of the R gene-dependent resistance is associated with HR where R proteins emit signals that feed into cell death pathways. However, in some cases HR-independent resistance has been observed. In tomato, Cf-9 codes for a membrane-anchored R gene providing resistance against *cladosporium fulvum* (**Jones et al., 1994**). The amount of R and avr protein or the duration of avr expression, determines whether resistance occurs with or without HR (**Shirasu and Schulze-lefert, 2000**).

HR, is highly complex defence response, along with the production of reactive oxygen species (**Lamb and Dixon, 1997**), modification of ion fluxes (**Levine et al., 1996**), is followed by activation of defence signal through the synthesis of signaling molecules such as jasmonic acid, salicylic acid and protein kinases (**Dangl et al., 1996; Dixon et al., 1994**). Salicylic acid collection leads to the onset of systemic acquired resistance in distal plant tissue (**Ryals et al., 1996**). These events are accompanied by the activation of several plant defense genes, local accumulation of pathogenesis related (PR) proteins, activation of transcription factors and degradation of proteins by the polyubiquitin system and cell death. These events limit the nutrient availability to the pathogens thereby restricting the spread of the pathogen (**Dixon and Harrison, 1990**).

MOLECULAR MARKER OF HYPERSENSITIVE RESPONSE

Although the molecular mechanism leading to the establishment of HR and active components of cell suicide still remains obscure, recent insight has been obtained in identification of useful genes which are activated during HR and are better known as marker gene of HR.

The tobacco *hsr203J* gene has been shown to be a molecular marker of the hypersensitive response (**Pontier et al., 1994**). The *hsr203J* gene is activated during the early steps of incompatible plant/pathogen interaction between tobacco and *R. solanacearum*. The analysis of the recombinant protein demonstrated that the *hsr203J* gene product is a serine hydrolase having esterase activity (**Baudouin et al., 1997**). The functional characterization of the gene product as an esterase, suggest either a role in the control of cell death, or a function in the establishment or limitation of cell death. The effect of other hypersensitive response (HR)-inducing pathogens and elicitors has been tested with transgenic plants containing the *hsr203J* promoter-GUS reporter fusion gene and the preferential inducibility of the *hsr203J* gene promoter during incompatible interaction was found (**Pontier et al., 1994**). Homologues of *hsr203J* has been found in tomato and the expression of *Cladosporium fulvum* avirulence *avr9* gene product in the tomato line containing the Cf-9 defense resistance gene led to rapid *hsr203J* gene activation. The relationship between the activation of *hsr203J* and cell death has been envisaged and expression of *hsr203J* gene has been found to be tightly correlated with programmed cell death (**Pontier et al., 1998**). Among potential effectors of HR such as SA, MeJ and INA, most of them were found to have effect on *hsr* gene expression in tomato (**Pontier et al., 1998**). The *hsr203J* gene is not activated during plant development and does not respond to classical elicitors such as fungal cell walls and its expression is dependent on the integrity of bacterial hypersensitive response and pathogenecity (*hrp*) genes (**Pontier et al., 1994**). The *P. solanacearum* isolate and harpin, a protein from *Erwinia amylovora* secreted via *hrp* genes are able to elicit an hypersensitive reaction in plants and are inducer of *hsr* gene (**Wie et al., 1992; Boucher et al., 1992**). Harpin was shown to trigger the expression of the *hsr203J*-GUS fusion in tobacco (**Pontier et al., 1994**). Histochemical GUS detection of tobacco leaves locally infiltrated with

Pseudomonas fluorescens with or without the *hrp Z* gene of *P. syringae* pv. *syringae* revealed the highly localized nature of the *hsr203J* in response to harpin (Pontier *et al.*, 1998). Similarly, in case of *R. solanacearum*, the *hsr203J* promoter induction was strictly confined to the inoculated site and depended on the presence of functional *hrp* genes. During an incompatible interaction between tobacco and the bacterial phytopathogen *Pseudomonas solanacearum*, *hsr201* and *hsr215* genes were expressed preferentially during hypersensitive reaction. The induction of these genes was confined to infected areas confirming its localised nature. Though HR is considered to be important element of plant disease resistance but with a necrotrophic pathogen like *Botrytis cineria*, the HR facilitates its colonization in the plant (Govrin and Levine, 2000). Although the HR is a common feature of many resistance reactions, it is not an obligatory component. Some resistance reactions, such as those mediated by the *mlo* gene of barley towards the fungus *Erysiphe graminis* f. sp. *Hordei*, precede the induction of a visible HR (Shira Su and Schulze-Lefert, 2000). The molecular mechanism behind the HR still remains unclear, although a few loci such as *eds-1*, *ndr-1* or *rar-1* (Century *et al.*, 1995; Parker *et al.*, 1996; Peterhansel *et al.*, 1997) involved in signaling pathways leading to HR have been identified. *eds-1* is a key component of disease resistance pathways activated by the TIR-NBS-LRR class of resistance genes in response to bacterial and oomycete pathogens. Antisense tobacco plants with reduced ascorbate peroxidase and catalase responsible for detoxifying ROS were found to be hyper responsive to pathogen attack (Mittler *et al.*, 1999). Antisense suppression of *hsr203J* in tobacco was found to accelerate the development of hypersensitive response in response to avirulent pathogens and a restriction of pathogen growth. Also a strong reduction of defense gene expression in cells undergoing HR was found (Tronchet *et al.*, 2001). *hsr203J*, identified and cloned in Brassica juncea is analyzed for its expression at different stages of infection in susceptible and tolerant genotypes and has been found to be associated with defence (Mishra A *et al.*, 2010).

Lesion-mimic mutants of *Arabidopsis* suggest the existence of genes involved in HR regulation (Lorrain *et al.*, 2003). LSD 1 expressed constitutively in plants coding for zinc finger protein is suggested to act as negative regulator of HR (Dietrich *et al.*, 1997). Nt LRP1 (*N. tabacum* Leucine Rich Protein 1) a tobacco gene has been found to have possible role as a modulator of the HR (Jacques *et al.*, 2006). Gain of function revealed that Nt LRP1 expression is induced early during the HR initiated by elicitors, *Ralstonia solanacearum* or Tobacco mosaic virus. Besides *hsr203J* there are few other marker genes for HR and Harpin-induced1 gene (*Hin1*) is one of them.

Besides *hsr*, several other genes, such as *Eli 3* (Kiedrowski *et al.*, 1992) and *AIG1* (Reuber and Ausubel, 1996) from *Arabidopsis thaliana*, or *hin1* from tobacco (Gopalan *et al.*, 1996), were also identified as pathogen-induced genes that are specifically activated by signaling molecules generated during an HR. *Eli 3* activation was found to be dependent on *RPM1* resistance locus. *Hin1*, isolated by subtractive hybridisation method has been found to be induced in a bacterial *hrp* gene-dependent manner, and in response to bacterial strains containing the *avr pto* gene.

Differential hybridization approach was used to isolate HIN1 (Gopalan *et al.*, 1996) and two closely *Hin1*-related genes as downstream target in the spermine-signaling pathway (Takahashi *et al.*, 2004). Spermine (spm), a major polyamine in plant transduces defense response and is identified as endogenous inducer of pathogenesis related-protein during TMV-induced HR. Pharmacological and biochemical analysis reveal that these marker genes are positioned downstream of spm-triggered mitochondrial malfunction (Takahashi *et al.*, 2004). Other marker genes, *hsr203J*, *HMGR*, *hsr201* and *hsr515* were also found to be spm-responsive. Experiments have revealed that the induction of *hin1*, *hsr203J* and *HMGR* genes by spm is independent of the SA-signaling pathway whereas expression of *hsr201* and *hsr515* was found to be partially dependent (Takahashi *et al.*, 2004).

ROLE OF ELICITORS IN HR

The aptness of some gram-negative bacterial pathogens, such as *Pseudomonas*, *Xanthomonas* and *Erwinia* strains, to cause disease in susceptible plants and elicit HR in resistant plants, is governed by the *hrp* (HR and pathogenicity) gene cluster (Bonas, 1994). *hrp* genes code for protein secretion pathway called type III secretion system (Van Gijsegem *et al.*, 1993). It was found that mutation in *hrp* gene leads to the elimination of the bacterium ability to cause disease in susceptible plants and to trigger resistance in resistant plants (Huang *et al.*, 1988). Harpins, a group of effector protein exported by the type III pathway of plants pathogenic *Erwinia*, *Pseudomonas* and *Ralstonia spp.* trigger HR (Galan and Collmer, 1999). Harpin has been reported to be expressed in tobacco only when it is produced in secretable form (Tampakaki and Panopvlos, 2000). Hypersensitive response-assisting protein (HRAP) is reported as an amphipathic plant protein isolated from sweet pepper that intensifies harpin_{pss} (harpin derived from *Pseudomonas Syringae pv syringae*)-mediated hypersensitive response (Chen *et al.*, 1998). The *hrap* gene is widely distributed in a broad range of plant species like tobacco, *Arabidopsis* and rice. The constitutive expression of *hrap* gene in transgenic tobacco plant enhances resistance against virulent bacterial pathogens by induction of a HR (Ger *et al.*, 2002). Constitutive expression of the *hrap* gene in *Arabidopsis* results in an enhanced disease resistance towards *E. carotovora subsp. carotovora*. The disease resistance against virulent pathogen was found to be harpin dependent. Different biochemical and molecular markers like ion leakage, H₂O₂, protein kinase, Athsr3 and Athsr4 were found to be induced (Pandey *et al.*, 2005). It was demonstrated previously that the harpin induced hypersensitive cell death is associated with altered mitochondrial function in tobacco cells (Xie and Chen, 2000).

ROLE OF REACTIVE OXYGEN SPECIES IN HSR

ROS are produced in plants through NADPH oxidases, amine oxidases and cell wall bound peroxidases and have been found to play role in biotic as well as abiotic stress. The generation of ROS in cell organelles like chloroplast and mitochondria are capable of inducing changes in the nuclear transcriptome, but the mechanism of signal transduction still remains unclear to some extent. In the chloroplast, plastoquinone (PQ), ascorbate, glutathione and ROS along with ferredoxin orthioredoxin system are the key signaling components (Pfannschmidt *et al.*, 1999 and Choudhury *et al.*, 2013). Peroxisomes are the major sites of H₂O₂ production thorough different biochemical reactions. During photosynthesis in C₃ plants, peroxisomes generate high amount of H₂O₂ that is light dependent and as such the antioxidant efficiency is extensively high in those organelles (Foyer *et al.*, 2003 and Choudhury *et al.*, 2013). These include enzymes like CAT, APX and those associated with ascorbate/glutathione system (Foyer *et al.*, 2003, Jimenez *et al.*, 1997 and Choudhury *et al.*, 2013). Depending on the nature of the ROS, some are highly toxic and are rapidly detoxified. Detoxification of ROS is one of the defense mechanism in plants and may occur via enzymatic or non enzymatic pathways. The non-enzymatic defense system of the plant comprises of a variety of antioxidant molecule-organic compounds such as amino acids (e.g Proline), quaternary and other amines (e.g. glycinebetaine and polyamines) and a variety of sugar and sugar alcohols (e.g. mannitol and trehalose), while the enzymatic one includes superoxide dismutase, ascorbate peroxidase, catalase, glutathione reductase and monohydroreductase. Antioxidant enzymes catalyze reactions that remove reactive oxygen species. Superoxide dismutase (SOD) converts O₂⁻ to H₂O₂ and then ascorbate peroxidase uses ascorbate as its specific electron donor to reduce H₂O₂ to water with concomitant generation of monodehydroascorbate (MDHA), a univalent oxidant radical of ascorbate. MDHA spontaneously disproportionates into di-dehydroascorbate (DHA) and ascorbate. Based on the requirements of metal cofactor SODs are classified into three

groups: Fe SOD, Mn SOD and Cu-Zn SOD. Fe SODs are located in the chloroplasts, Mn SODs are in mitochondria and peroxisomes and Cu-Zn SODs in the chloroplasts, the cytosol and the extracellular (apoplast) space (Alscher *et al.*, 2002 and Kar, 2011). MDHA can also be directly reduced to ascorbate by the action of NAD(P)H-dependent monodehydroascorbate reductase (MDHAR). Dehydroascorbate reductase (DHAR) uses reduced form of glutathione (GSH) to reduce DHA and thereby regenerate ascorbate. The oxidised glutathione (GSSG) is then converted to reduced glutathione by glutathione reductase (GR), by using NAD(P)H as the reducing power (Asada, 1992).

Whereas plants are glut with mechanisms to combat increased ROS level during abiotic stress conditions, in other circumstances plants appear to purposefully generate ROS as signaling molecule to control various process including pathogen defense and programmed cell death. The suppression of ROS detoxifying mechanism is crucial for the onset of PCD. Biotic stress results in the activation of NADPH oxidase and the repression of ascorbate peroxidase and catalase by salicylic acid and NO which leads to the overaccumulation of reactive oxygen intermediates (ROI) and activation of defense mechanism (Klessig *et al.*, 2000). On the contrary, during abiotic stress, ROI-scavenging enzymes ascorbate peroxidase and catalase are induced to reduce the ROI level. Several roles for ROS during pathogen infections have been proposed: as direct antimicrobial agents, as activators of defense genes, as agents for cross linking proteins to limit pathogen infections (Bolwell *et al.*, 1995) and as producers of HR, cell death, SA production and SAR (Lamb and Dixon, 1997).

The accumulation of reactive oxygen intermediates is a rapid event upon pathogen attack that precedes cell death in incompatible R gene triggered resistance reaction (Levine *et al.*, 1994). The ROI have dose-dependent antagonistic action i.e. depending on the concentration of ROS three distinct phases characterize cellular responses to the oxidative stress (Levine *et al.*, 1994). Low doses induce antioxidant enzymes like glutathione peroxidase; however, when the concentration of ROS reaches a certain threshold a signal transduction pathway that results in R-gene-dependent PCD, is activated (Levine *et al.*, 1996). High doses results in necrosis. More molecular and genetic studies are referred to confirm the role of oxidative burst in the cell death.

H₂O₂ AS A SIGNAL FOR HSR

During oxidative burst O₂⁻ generated by a multi-subunit NADPH oxidase complex in the plasma membrane shows analogy to the oxidase in mammalian phagocytes and O₂⁻ is rapidly dismutated to H₂O₂ (Doke *et al.*, 1996). In plants massive oxidative burst that generate high level of H₂O₂ have been observed in response to avirulent pathogen as part of the HR (Legendre *et al.*, 1993; Lamb and Dixon, 1997). It was shown that enhanced H₂O₂ production during the HR led to dramatic increase in amount of cell death in a soybean cell culture system (Levine *et al.*, 1994). However, when the role of ROS was investigated during the induction of TvX-triggered hypersensitive cell death it was suggested that production of ROS is not always necessary and the signal-transduction pathway leading to cell-death may exist independent of oxidative burst. Similar result was found during the *hsr203J* gene activation in tomato and H₂O₂ and related metabolites were not found to play major role in the cell death, even at high concentration. It was suggested that a pathway not requiring ROS is involved or the ROS is insufficient as a cell death activator (Pontier *et al.*, 1998). It was also observed that the signaling pathway might involve a serine protease (Yano *et al.*, 1999). The role of H₂O₂ accumulation and hypersensitive cell death in barley against powdery mildew fungus was studied and a positive association between hypersensitive response mediated cell death and H₂O₂ production was observed. However, there was no accumulation of SA indicating that the salicylic acid is not provoked during cell death in barley (Huckelhoven *et al.*, 1999). ROS have

been shown to influence the expression of a number of important MAP kinases which phosphorylate a variety of substrates including transcription factors, other protein kinases, cytoskeleton-associated proteins and several stress associated genes, indicating a direct connection with the stress response, further complicated by the fact that ROS production can also be controlled by a MAP kinase cascade (Pitzschke and Hirt, 2006; Ren *et al.*, 2002). The effect of H₂O₂ on MAP kinase activation was also investigated by Kovtun *et al.* (2000) using *Arabidopsis* protoplast, and these workers found that it activated two MAP kinase of 42 and 44kDa. H₂O₂ generation occurs both locally and systemically in response to wounding. Recent work shows that H₂O₂ functions as a second messenger mediating the systemic expression of various defense related genes in tomato plants (Orozco-Cardenas *et al.*, 2001). Previously, it was found that the oxidative burst in pathogen challenged *Arabidopsis* leaves activates a secondary systemic burst in distal part of the plant, leading to systemic immunity *via* the expression of defense related genes (Alvarez *et al.*, 1998).

Role of MAP Kinases

Extensive research has been done to elucidate the components of the pathway leading to the defense response. MAP kinase, member of serine/threonine protein kinase has been found to be an important component of signal-transduction pathway and is present in all eukaryotes. The cascade includes MAP kinase, MAP kinase kinase and MAP kinase kinase kinase. Active MAP kinase requires phosphorylation on tyrosine and threonine in the conserved threonine-X-tyrosine (TXY) sequence in kinase subdomain VIII (Peyne *et al.*, 1991). A growing body of evidence suggest that MAP kinase cascades operate in plants. MAP kinases have been implicated in regulating certain aspects of plant growth and development, including cell division, hormone action and pollen development (Hirt, 2000; Tena *et al.*, 2001; Zhang and Klessig, 2001). Various biotic and abiotic stresses also activate plant MAP kinase.

Mitogen-activated protein kinase (MAPK) signaling plays central roles in intracellular immunity pathways. Stimulus-triggered activation of a MAP kinase kinase kinase (MAP3K; also called MEKK) initiates MAP kinase signaling (Magnus *et al.*, 2012). PRR directly or indirectly affect MAP3K activation, which in turn leads to the phosphorylation and thus the activation of downstream MAP kinase kinases (MAP2K; also called MKK or MEK) (Magnus *et al.*, 2012). Molecular and biochemical analysis suggest that plant defense response involves MAP kinase activities (Romeis *et al.*, 1999). Plant homolog for all three components of this cascade has been identified (Mizoguchi *et al.*, 1998). Evidence that MAP kinase regulate innate immunity in plants has come from several studies. MAP kinase play role in signaling gene-for-gene interaction-dependent defense response. It was found that tobacco cells, expressing the tomato *cf-9* resistance gene, respond to *avr 9* protein from the fungal pathogen *Cladosporium fulvum* by activation of MAP kinase (Romeis *et al.*, 1999). Treatment of tobacco suspension cultured cells with a fungal elicitor, derived from the cells walls of *Phytophthora infestans* resulted in the transient activation of a 47KDa MAP kinase (Suzuki and Shinshi, 1995). MAP kinase 4 was hypothesized to function as a negative regulator of SAR. Evidence shows that MPK4 mutant in *Arabidopsis* exhibit constitutive SAR. Loss of MAP kinase 4 function leads to increased SA levels and exhibits enhanced resistance to virulent pathogens (Petersen *et al.*, 2000). In addition to repressing SA-mediated defense, MPK4 is required for JA mediated gene expression. MAP kinase 4 may therefore, be involved in integrating SA and JA-dependent responses to selectively engage defenses against particular pathogen types or environmental stresses (Felton *et al.*, 1999; Pieterse and van Loon, 1999). Similarly, a portion of MAP kinase cascade that positively regulates defense response was identified in *N.tabacum* (Yang *et al.*, 2001). In tobacco two distinct member of MAP kinase is involved in the defense gene expression and HR like cell death against Tobacco mosaic virus. They are SA-induced protein kinase (SIPK) (Zhang and Klessig, 1997) and wound-

induced protein kinase (WIPK) (Takahashi *et al.*, 2003). SIPK is also activated by treatment of tobacco cells with different elicitors like parasiticein, cryptogein and a cell wall derived elicitor from the pathogenic fungus *Phytophthora parasitica* (Zhang *et al.*, 1998). WIPK activation by TMV was found to depend on the disease-resistance *N*-gene and is an important component upstream of salicylic acid in the signal transduction pathways leading to local and systemic resistance to TMV (Zhang and Klessig, 1998). Nt Mek2, a MAP kinase upstream of both SIPK and WIPK was isolated (Yang *et al.*, 2001) from tobacco. Expression of constitutively active Nt MEK2 (a MAP kinase kinase) led to the activation of SIPK and WIPK and, subsequently, induced HR-like cell death and defense gene expression. Gain of function and loss of function studies on MAP kinase cascade members reveal that the expression of spm-induced HR marker genes varies with respect to involvement of SIPK/WIPK activation. A complete *Arabidopsis* MAP kinase cascade, consisting of MEKK1, MKK4/MKK5 and MPK3/MPK6, that is activated in response to a 22-amino acid peptide derived from bacterial flagellin (flg22) was recently identified (Asai *et al.*, 2002). Transient over-expression of constitutively activated MEKK1, MKK4 or MKK5 in *Arabidopsis* leaves enhanced resistance to bacterial and fungal pathogens, suggesting that this MAP kinase cascade plays an important role in signaling defense response. More than twenty MAP kinases have been cloned or genomically annotated in *Arabidopsis*, although their specific functions remain unclear (Mizoguchi *et al.*, 1997). These MAP kinases presumably act downstream of three major classes of putative MAP kinase kinase kinase typified by CTR1, ANPS and MEKK1. Yeast two-hybrid experiments show that MPK4, the MAP kinase kinase, AtMKK2, AtMEK1 and the MAP kinase kinase kinase, AtMEKK1 interact (Ichimura *et al.*, 1998). The *Arabidopsis* homologues of WIPK and SIPK appear to be ATMPK3 and ATMPK6 respectively. Bacterial, fungal and plant derived defense response elicitors induced 45 and 49kDa MBP kinase activity in *Arabidopsis* suspension cultures cells and leaf tissues. Loss-of-function approach demonstrated that *Arabidopsis* MAP kinase 6 plays a role in resistance to certain pathogen. Silencing of MAP kinase 6 showed no apparent morphological phenotype or reduced fertility, indicating MPK6 is not required for development. Despite that, resistance to an avirulent strain of *Peronospora parasitica* and *Pseudomonas syringae* were compromised revealing its role in both resistance-gene mediated resistance as well as basal resistance (Menke *et al.*, 2004).

It appears that plant MAP kinase pathway is not neatly delineated into separate parallel cascades. Some MAP kinases are known to be activated by common upstream elements, for example ATMPK3 and ATMPK6 by ANP1 through oxidative stress (Kovtun *et al.*, 2000). However, although ATMPK4 and ATMPK6 share many similarities in their activation by stresses such as wounding (Ichimura *et al.*, 2000). ANP1 will not activate ATMPK4 which is thought to be activating ATMEKK1 (Ichimura *et al.*, 1998). Expression of MAP kinases during pathogenesis of Alternaria blight in mustard suggests that the signalling pathways might be differentially modulated by the pathogen to facilitate its colonization during different stages of infection (Mishra A *et al.*, 2015). Hence, these MAP kinases could be attractive targets for genetic manipulation in order to develop resistant lines of Brassica (Mishra A *et al.*, 2015).

ROLE OF SALICYCLIC ACID IN HR

Salicylic acid (SA), a phenolic compound (ortho-hydroxy benzoic acid) plays an important role in induction of plant defense against a variety of biotic and abiotic stresses through morphological, physiological and biochemical mechanisms (Abdul *et al.*, 2011). SA synthesized by plants in response to a wide range of pathogens, and is essential for the establishment of local and systemic resistance (Loake and Grant, 2007; Vlot *et al.*, 2009). The importance of SA arises

from its role in the mediation of resistance (*R*)-gene resistance and basal immune responses, and from the positive link between SA-mediated defence and the small interfering RNA (siRNA) antiviral machinery (Alamillo *et al.*, 2006; Baebler *et al.*, 2014; Hunter *et al.*, 2013).

The HR-mediated cell death is related to the induction SA known for pharmacological use were found to affect cell growth, differentiation and inflammation (Pillinger *et al.*, 1998). Plants were found to synthesize SA and activate SA-dependent physiological processes (Klessig and Malamy, 1994). Later on it was found that SA has a role as signaling molecule and is involved in disease resistance and PCD (Delaney *et al.*, 1994). Exogenous SA application induces defense genes, phytoalexin production and promotes ROS generation and PCD (Shirasu *et al.*, 1997). A large body of evidence suggest the role of SA in disease resistance and SA is known to induce systemic acquired resistance in plants (Ryals *et al.*, 1996). SAR is a general defense mechanism that activates in response to a pathogen that causes a necrotic lesion either as a consequence of HR or as a result of disease symptom development in the course of a compatible interaction (Hammerschmidt, 1999) in the distal, uninfected parts and is effective against a broad spectrum of microbial pathogens. SA activates the SAR regulatory protein, nonexpressor of PR genes (NPR1) through redox changes, which in turn drives systemic expression of PR proteins and facilitates their secretion by upregulating protein secretory pathway genes (Wang *et al.*, 2005). Lipid metabolism also plays a central role in SAR signaling (Nandi *et al.*, 2004). A peptide signal system mediated by the Asp protease constitutive disease resistance 1 (CDR1) appears to be essential for SAR long-distance signaling in *Arabidopsis* (Xia *et al.*, 2004). of defense response and establishment of SAR that immunizes the entire plant against further infection. Recent data suggest a complex role of SA and an involvement in the activation of HR at primary infection sites. Transgenic *NahG Arabidopsis* plants expressing a bacterial SA hydroxylase lose the ability to induce SAR and PR gene expression suggesting the role of SA in SAR (Delaney *et al.*, 1994). SA accumulation itself is positively regulated. It potentiates induction of phenyl alanine ammonia-lyase (PAL) a key enzyme in SA synthesis. *Arabidopsis* constitutive SAR mutant *hrl1* was used to understand the regulation of HR against pathogen in plants and it was observed that pre-existing systemic acquired resistance negatively regulates HR-associated cell-death (Devdas and Raina, 2002). Recent studies show that H₂O₂ functions upstream of SA in development of SAR and induces SA accumulation. SA promotes *PR* gene induction in distal part of plant, enhancing defense and limiting pathogen growth. LSD1 gene, coding for novel Zinc finger protein in *Arabidopsis* functions as a negative regulator of plant cell death (Dietrich *et al.*, 1994). Plant defense signal molecule SA induces rapid inhibition of ATP synthesis in tobacco cell cultures. SA has been found to affect MAP kinase (SIPK) defense.

Besides SA, NO also plays an important role in defense gene induction and HR mediated cell-death (Delle donne *et al.*, 1998; Durner *et al.*, 1998). NO synthase (NOS) activity was found to be enhanced upon TMV-triggered and *R*-gene-dependent HR in tobacco (Durner *et al.*, 1998).

ROLE OF MITOCHONDRIA IN HR

Mitochondrion has found to play important role in the expression of HR associated PCD in plants. The HR/inducing bacterial virulence factor *harpin* disrupts mitochondrial function, and HR like cell death and disease resistance marker gene expression can also be activated in plant cells in which *Bax* is expressed from a viral vector. At present, it is not clear whether cytochrome c leakage also occur during HR although leakage has been observed in plant cell undergoing PCD in response to other inducer. Further evidence for the involvement of plant mitochondria in the

regulation of HR-associated cell death comes from studies of the alternative oxidase (AOX), an IMM (inner mitochondrial membrane) enzyme that is not found in animal mitochondria. AOX catalyses electron flow directly from ubiquinol to oxygen, thereby creating an electron shunt that bypasses complex III and IV of the IMM and results in a cyanide insensitive electron-transfer pathway. AOX activation by treatment with cyanide during the HR may help to suppress cell death during the propagative phase of lesion formation and thus restrict the size of the necrotic zone (**Chivasa and Carr, 1998**). However, over-expression of AOX has the reverse effects, providing supporting evidence for a model in which plant mitochondria have an important role as a signal generator for HR induce cell death, perhaps by generation of ROS derived from electron-transfer intermediate in the IMM (**Lam et al., 1999**). In plants, the mitochondrion is not the only compartment in which ROS can be generated. In addition to a plasma membrane-localized NADH oxidase, the plastid organelles can also participate in HR-associated cell death signaling. Recently, the plastid-localized protein DS9 was found to regulate the rate of HR cell death in the N gene/ TMV system (**Seo et al., 2000**). Overexpression of DS9 led to a delay of cell death activation by TMV. Mitochondria play an important role in ROS generation leading to LCD in mammalian cells, and recent observations suggest a similar role in plants (**Maxwell et al., 2002, Amirsadeghi et al., 2006, Love et al., 2008 and Matias et al., 2010**). For instance, treatment of Arabidopsis leaves with bacterial elicitors results in rapid ROS generation in mitochondria, followed by membrane pore formation, dissipation of membrane potential and decline of ATP levels (**Matias et al., 2010**). The results indicate that oxidative phosphorylation is uncoupled early after the challenge, leading to decrease in oxygen consumption and ROS propagation (**Matias et al., 2010 and Yao et al., 2006**). Mitochondria produce ATP via respiratory oxidation of organic acids and transfer of electrons to O₂ via the mitochondrial electron transport chain (**Huang et al., 2016**). This cycle produces reactive oxygen species (ROS) at various rates that can impact respiratory and cellular function, affecting a variety of signalling processes in the cell (**Huang et al., 2016**). Roles in redox signaling, retrograde signaling, plant hormone action, programmed cell death, and defense against pathogens have been attributed to ROS generated in plant mitochondria (mtROS) (**Huang et al., 2016**).

ROLE OF PROGRAMMED CELL DEATH IN HR

Programmed Cell Death (PCD) is a genetically determined process present in all multicellular organisms by which cells activate their own death (**Vaux and Korsmeyer, 1999; Lam et al., 1999**). It is a biological process that functions in many aspects of animal and plant development and their response to stress.

In plants, during the tracheary elements differentiation (**Kuriyama and Fukuda, 2002**), aerenchyma formation (**Gunawardena et al., 2001**), hypersensitive response (**Heath, 2000**) and as a consequence of several biological and chemical stresses (**Beers and Mc Dowell, 2001**) PCD has been observed. When a pathogen invades a plant, two types of cell death responses are mounted on the plant side. If the plant is resistant to the pathogen, a rapid cell death is frequently triggered at the primary site of infection, which constitutes the hypersensitive response (HR) and is accompanied by activation of local defense response (**Heath, 2000**). If the plant is susceptible, disease develops, and slower cell death develops as local and systemic infection progresses. Cell death associated with the HR may be only one of the larger set of cellular responses that are co-ordinately activated by different stress signals. Isolation of spontaneous cell death mutants in *Arabidopsis* and maize, in which PCD is activated in the absence of pathogens or stress, suggests that PCD in plants is under genetic control (**Dietrich et al., 1994; Greenberg et al., 1994**). The cell death component of the HR may function more as a signaling system than as a direct defense mechanism (**Heath, 2000**). Concomitant with the onset of the HR, there is transcriptional activation of defense genes encoding enzymes of phytoalexins and lignin synthesis, lytic enzymes, and

other antimicrobial proteins as part of a massive switch in host gene expression. The expression of *hsr 203J* and its correlation with cell death through accumulation of proteases and protease inhibitors in tolerant and susceptible genotypes during pathogenesis of *Alternaria* blight in Brassica has been reported. (Mishra A *et al.*, 2011).

CONCLUSIONS

- Breeders have often used resistance genes to introduce resistance in their crops, and with a few exceptions, all introgressed resistance genes have been shown to lack durability in the field (Pink and Puddephat, 1999). Pathogens are usually able to overcome resistance gene-mediated recognition either by shedding the corresponding elicitor gene, or by accumulating mutation in the gene, which prevents the gene product from being recognized, and thus fails to trigger the HR.
- The antimicrobial defence of multicellular organisms is thought to involve the activation of suicide pathway in infected cells termed as hypersensitive response.
- The correlation between HR related cell death during initial phase of infection and induction of MAP kinase machinery during pathogenesis will enable to provide the molecular insights for engineering resistance against several disease.
- The wide spectrum of defence responses has prompted research of defense responses to identify and use signal transduction “master switches” to engineer disease resistance. The *Arabidopsis NIM 1/NPR1* gene seems to be crucial in salicylic acid mediated resistance, and overexpression leads to resistance against several pathogens (Cao *et al.*, 1998). Other enhanced disease resistance (*edr*) mutants have been identified. Constitutive induction of an HR has been achieved in mutants of *Arabidopsis* and has been shown to coincide with elevated pathogen resistance (Dietrich *et al.*, 1994). But engineering resistance through the use of these master switches is generally not without drawbacks. Most mutants possessing constitutive expression of a defense pathway show reduced yield or plant vigour. Efforts have been made to generate transgenic plants that express the introduced gene under controlled condition only. This involves transfer of a pathogens-derived elicitor gene to the plant, expression of which is made conditional on pathogen infection by putting it under control of a tightly regulated pathogen inducible promoter. Strategies have been developed for creating novel disease resistance traits whereby transgenic plants respond to infection by a virulent pathogen with the production of an elicitor. Pathogen-induced elicitor production in transgenic tobacco generated a hypersensitive response and non specific disease resistance (Keller *et al.*, 1999). Transgenic tobacco plants harbouring a fusion between the pathogen-inducible tobacco *hsr203J* gene promoter and a *Phytophthora cryptogea* gene encoding elicitor cryptogenin was generated. Upon infection cryptogenin was found to be induced (Keller *et al.*, 1999). The transgenic plants showed hypersensitive response broad spectrum disease resistance. Thus exploitation of the HR by genetic means might be a strategy for creating novel disease resistance traits.

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